FIGURE 1A-1

AGA AGA A TT THE STANFORM OF THE STANFORM O ALT ACA FGA 5 5 5 SCA SCA AAC GCG TITC S S S 37G THE SAME THE CCT THE STATE OF AGC GGG GGG HAYCH ACCEPTANCE OF ACCEPTANCE SAG NGT HAGE REPORTED TO THE PROPERTY OF THE PROPERTY CCT CTG CGG

FIGURE 14-3

IGURE 14-4

AAA ATG GRANGER OF STATE OF S ATT I GGT A A CCAC Y Y Y Y Y Y CCAT H H H H H H CCAC CCAT CCAT CCAT CCAT CCAT CCAT CCAC GAC AGA ACT TGC TIA TAT ATG

H

CTT

CGT

D

D

CCA

CCA

R

ATG

ATG

AATG

A

FIGURE 1B

TTTTTAAGAA CACAATATAT TANGCATTAT CCATCTTATT AGTGTGGAGC TGTGGAAAGA ATGCTGAAGT ACAAATGAGA ATCCAAAGTA TTCTGTCACT AATTTTCAGA ATAAAATTAG GCAAATCAGT AATTTTCATT GGTAAGGAAA ATNTACCAAT GTTGGGCAGA ATTATANTCC CATTGAACTC CCAGTCTCAG

FIGURE 1C

58	112
57	118
57	108
57	107
58	115
58	50
-MAEGNHRKKPIKVIESIGKDFITGVIDNIVEQNVINWKEBEKKKYYD-AKTEDKVRVMA 58 -MADKULKEKRKIFIRSMGEGTINGILDEILQTRVINKERMEKVKREN-ATVMDKTRALI 58 -MASUDDISLIRKNRMALFQQITCVIPIIDNILKANVINKQEHDIIKQKTQIPLQARELI 58 -ESNDILLIRKNRMALFQUHTCVIPIIDSLITAGIINEQEHDVIKQKTQTSLQARELI 57 -MHPHQETIKKNRVVLAKQIILSELILEHDIITLERDIITLEMBLIQAKVGSFSQNVELL 57LVDKLLVRDVIDKCMERELITIENDIITLAMBLIQAKVGSFSQNVELL 57LVDKLLVRDVIDKCMERELITIENDRNIAAARNNGNESGVRELI 44 MEARDKQVLRSIRIELGAEVLVEGIVIQXIYQEGILTENHIQEINAQTTGLRKTMLLI 58	DSMQBKQRWAGQMILQTFFNIDQISPNKKAHPNWEAGPPESGESTDALKLCPHE 112 DSVIPKGAQACQICITYICEEDSYLAGTIGISAAPQAVQDNPAMPTSSGBRGNVKICSLE 118 DT'ILVKGNAAANIFKNGLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSIEBE 108 DT'ILVKGNIAATVFRNSIQBARAVIY
ICH-2	ICH-2
ICE	ICE
IAP1-453	IAP1-453
IAP2-439	IAP2-439
ICH-1	ICH-1
ICH-1	mda5-125

REPLACEMENT DRAWING SHEET

FIGURE 1D-1

	14 23 120	28 49 180	87 240	51 1113 300	102 169 358	117 184 418
eIF4A1 p68RNAhelicase Mda-5 eIF4A1 p68RNAhelicase Mda-5	LILSTIEKGVWHIGWTREFVEALRRIGSPLAARYMNPRITDIPSPSFRNHDBYLQLIND:	LQPTLVDKLLVRDVLDKCMEBELLTIRDRNRIAAAENNGNESGVRELLKRIVQKEWFSA	BL	KIVDSFDDMNLSRSLLRGIYAYG NCPKPVLNFYBANFPANVMDVIARQN BNNSSESSFADSSVVSESDTSLARGSVSCLDESLGHNSNMGSDSGTMGSDSDERNVAARA		
	eIF4Al p68RNAhelicase Mda-5	eIF4Al p68RNAhelicase Mda-5	eIF4Al p68RNAhelicase Mda-5	eIF4Al p68RNAhelicase Mda-5	eIF4Al p68RNAhelicase Mda-5	eIF4A1 p68RNAhelicase Mda-5

REPLACEMENT DRAWING SHEET

FIGURE 1D-2

p68RNAhelicase Mda-5	NSLINLENGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPV 478	120 187 478
elF4Al p68RNAhelicase Mda-5	MALGDYMGASCHACIGGTNVRABVQKLQMBÄPHIVGTPGRVFDMLNRRYLSPKYIKMFV 180 ABYCRACRLKSTCIYGGAPKGPQIRDLBRG-VBICIATPGRLIDFLBCGKTNLRRTTYLV 246 IPLPQILGITASPGVGGATKQAKAEBHILKLCANLDAFTIKTVKBNLDQLKNQIQBPCKK 538	180 246 538
eIF4A1 p68RNAhelicase Mda-5	LDBADBMLSRGFKDQIYDIFQKLNSNTQVVLLSATMPSDVLBVTKKFMRDPIRLLVKKBB 24 LDBADRMLDMGFBPQIRXIVDQIRPDRQTLMWSATWFKEVRQLAEDFIKDYIHINIGALB 30 FAIADATREDPFKEKLLEIMTRIQTYCQMSPMSDFGTQPYEQWAIQMEKKAAKKGNRKER 59 :	240 306 598
eIF4Al p68RNAhelicase Mda-5	LTLEGIRQF	65 31 58
eIF4A1 p68RNAhelicase Mda-5	DEDDLKKPLKLDETDRFLMTLFFENNKMLKRLAENPEVENEKLTKLRNTIMEQYTRTEES 718	73 41 18
elr4Al p68RNAhelicase 4da-5	-QAVIFINTRRKVDWLTEKMHARDFTVSAMHGDMDQKERDVIMREF 318 NKTIVFVETKRRCDELTRKMRRDGWFAMGIHGDKSQQERDWVLNEF 387 ARGIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPWTQNEQKEVISKF 778	18 37 18

FIGURE 1D-3

eIF4Al p68RNAhelica: Mda-5	
a v z	

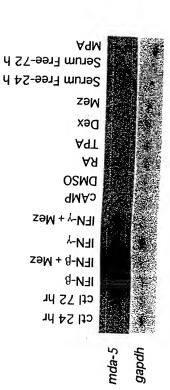
eIF4Al p68RNAhelicase Mda-5

371	406
440	500
838	898
RSGSSRVLITTDLLARGIDVQQVSLVINYDLPTNRENYIHRIGRGGRFGRKGV 371 KHGKAPILIATDVASRGLDVEDVKFVINYDYPNSSEDYIHRIGRTARSTKTGT 440 RTGKINLLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGS 838 : *. :**;* : .*;*::::::**.*.	AINMVTEEDKRTLRDIETFYNTSIEEMPLNVADLI

FIGURE 2A







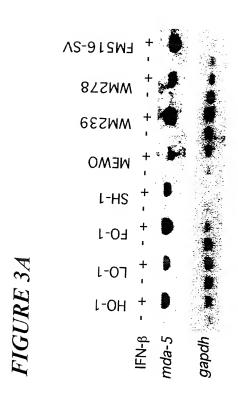
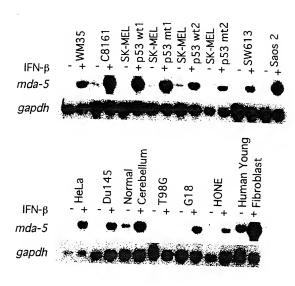
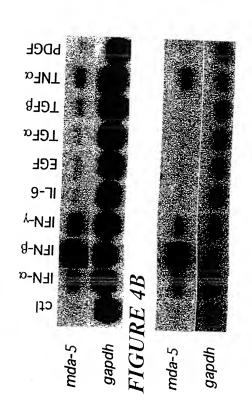


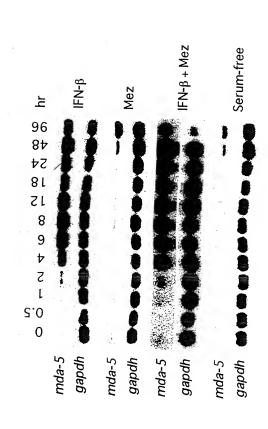
FIGURE 3B











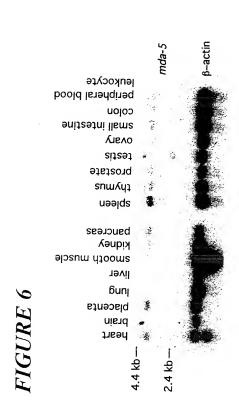
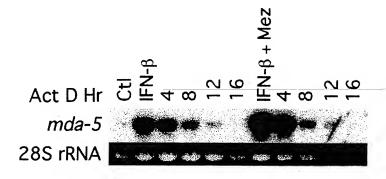


FIGURE 7A



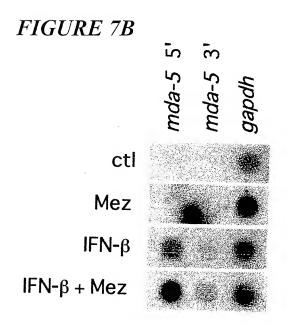
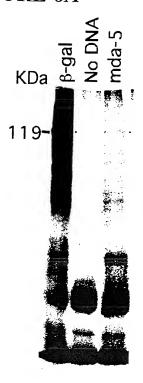
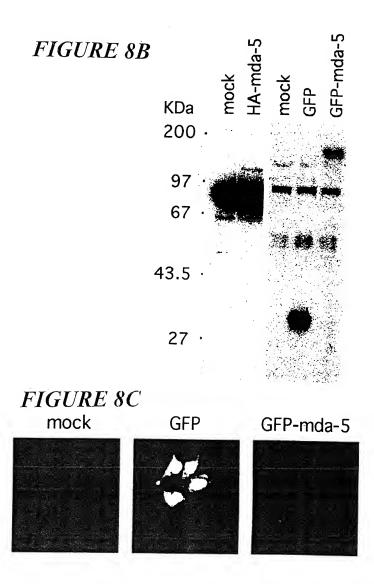
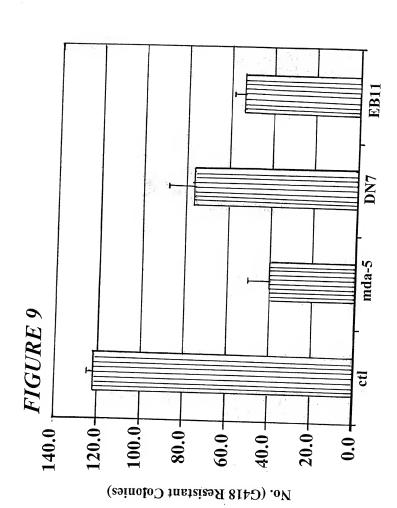


FIGURE 8A







REPLACEMENT DRAWING SHEET

	FIGURE 10	
;	GCACATTTTGGCCTACAAAGGACCTTATTGTTAAGGCAGAACCTGCTGGGAAAACAAAAT 1	60
	EcoRI	
6:	ATCCGCCGGAGGAGCTTTGTAGAGCGTTGGTCTTGGTGTCAGAGAGAATTCGCTTTCCTT	120
121	TTCTGTTTCCCGCGGTGTCCTTAACCAAAGGCCTCCTCTCTTCACCCGCCCCGACCAAAA	180
181	GGTGGCGTCTCCCTGAGGAAACTCCCTCCCCGCCAGGCAGATTACGTTTACAAAGTCCTG	240
241	AGAAGAGAATCGAAACAGAAACCAAAGTCAGGCAAACTCTGTAAGAACTGCCTGACAGAA	00
301	AGCTGGACTCAAAGCTCCTACCCGAGTGTGCAGCAGGATCGCCCCGGTCCGGGACCCCAG	60
361	GCGCACACCGCAGAGTCCAAAGTGCCGCGCCTGCCGGCCG	20
421	GCGCGCCGCCCGCTGCCCACCTGCCCACCTGCCCAGGTGCGAGTGCAGCCC	80
481	CGCGCGCCCGGCCTGAGAGCCCTGTGGACAACCTCGTCATTGTCAGGCACAGAGCGGTAGA	40
541	CCCTGCTTCTNTAAGTGGGCAGCGGACAGCGCACACATTTCACCTGTCCCGCAGACA	00
	BstXI	
601	ACAGCACCATCTGCTTGGGAGAACCCTCTCCCTTCTCTGAGAAAGAA	50
661	GTATTCCACAGACGAGAATTTCCGCTATCTCATCTCGTGCTTCAGGGCCAGGGTGAAAAT	20
721	GTACATCCAGGTGGAGCCTGTGCTGGACTACCTGACCTTTCTGCCTGC	30
781	GCAGATTCAGAGGACAGTCGCCACCTCCGGGAACATGCAGGCAG	0 1
	EcoRI	
841	CACCTTGGAGAAGGGAGTCTGGCACCTTGGTTGGACTCGGGAATTCGTGGAGGCCCTCCG	0
	Saci	
901	GAGAACCGGCAGCCCTCTGGCCGCCCCCCTACATGAACCCTGAGCTCACGGACTTGCCCTC	0
961 -	TCCATCGTTTGAGAACGCTCATGATGAATATCTCCAACTGCTGAACCTCCTTCAGCCCAC	0
В	HindIII	
1021	TCTĠGTGGACAGCTT + 1036	

